

SEQUENCE LISTING

<110> Tsukahara, Kappei
 Tsuchiya, Mamiko
 Jigami, Yoshifumi
 Nakayama, Kenichi
 Umemura, Mariko
 Okamoto, Michiyo

<120> METHOD OF SCREENING FOR COMPOUNDS THAT
 INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

<130> 082368-004400US

<140> 10/536,935
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<150> PCT/JP03/14909
<151> 2003-11-21

<150> JP 2002-339418
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<170> FastSEQ for Windows Version 4.0

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Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn
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gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg 144
Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
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aaa aat tcc aac ctt atg cct ggc att tcc agc gtg caa tac ata 192
Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile
50 55 60

att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att 240
Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Ser Ile Thr Ile
65 70 75 80

tat gct agt gaa cca tac ctt cta aac acg cta ata ctg tta cct tgt 288
Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Pro Cys

85	90	95	
ttg ctc gca ttc ata tat gga aaa ttt act agc tcg agt aaa cct tct Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser 100	105	110	336
aat cca ata tac aat aaa aaa atg att aca cag cggttccaa cta Asn Pro Ile Tyr Asn Lys Lys Met Ile Thr Gln Arg Phe Gln Leu 115	120	125	384
gaa aaa aag ccgttatattactgcgttatcggtgggatgttttattctg Glu Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu 130	135	140	432
act gct att gcc atc ttg gct gta gat ttt cca att ttc cca agg agg Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg 145	150	155	480
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gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu 180	185	190	576
aaa aac cta agc ttg a'ag agt aaa ccc agc ttc tta aaa aat gca ttt Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe 195	200	205	624
aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg 210	215	220	672
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ggg gtt cat tgg aat ttt ttc acc cta tca ttg ttg cca ctt gta Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val 245	250	255	768
ttg acc ttt att gat ccc gtc aca aga atg gtt cca cgc tgc tca att Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile 260	265	270	816
gca ata ttc att tca tgc att tat gaa tgg cta ctt tta aag gac gat Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp 275	280	285	864
cgc act tta aac ttt tta -att ttg gct gat aga aat tgt ttc ttc agt Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser 290	295	300	912
gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe 305	310	315	960
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tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser	340	345	350	1056
aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser	355	360	365	1104
ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val	370	375	380	1152
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tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val	420	425	430	1296
gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu	435	440	445	1344
ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile	450	455	460	1392
gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser	465	470	475	1440
ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile	485	490	495	1488
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Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
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Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile
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Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys
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Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Lys Pro Ser
100 105 110

Asn Pro Ile Tyr Asn Lys Lys Met Ile Thr Gln Arg Phe Gln Leu
115 120 125

Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Met Leu Ile Leu
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Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg
145 150 155 160

Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val
165 170 175

Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu
180 185 190

Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe
195 200 205

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225 230 235 240

Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val
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260 265 270

Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Lys Asp Asp
275 280 285

Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser
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Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe
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Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr
325 330 335

Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser
340 345 350

Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
355 360 365

Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
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 Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
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 Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
 420 425 430
 Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
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 450 455 460
 Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
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 Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
 20 25 30
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 Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
 35 40 45
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 Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
 50 55 60
 att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240
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 65 70 75 80
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 Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
 85 90 95

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Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu			
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Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro			
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Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu			
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gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa		528	
Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln			
165	170	175	
ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat		576	
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Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val			
245	250	255	
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Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala			
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Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val	

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Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln			
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Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr			
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Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
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Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
420 425 430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile
435 440 445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
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Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
20 25 30

tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
35 40 45

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Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
50 55 60

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65 70 75 80

att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
85 90 95

tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa 336
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
100 105 110

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gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln 165	170	175	528
ttg atc aag aac cac acc gac aat tac aaa ttt agt tgg aag agt tat Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr 180	185	190	576
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tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu 210	215	220	672
cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Thr Leu Gly 225	230	235	720
ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val 245	250	255	768
cca cgc ttc ata ata gga att ggt atc tca att ggt tat gag gta gcg Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala 260	265	270	816
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ctt gaa tct ctc atc gcc atg aat aaa gaa ggt att ttt tcg ttt att Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile 290	295	300	912
gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val 305	310	315	960
tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile 325	330	335	1008
cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser 340	345	350	1056
gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu 355	360	365	1104

gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser	370	375	380	1152
aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn	385	390	395	400
gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly	405	410	415	1248
aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe	420	425	430	1296
atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile	435	440	445	1344
aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly	450	455	460	1392
tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys	465	470	475	480
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<213> Candida albicans

<400> 6				
Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu	1	5	10	15
Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu	20	25	30	
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu	35	40	45	
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser	50	55	60	
Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val	65	70	75	80
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro	85	90	95	
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu	100	105	110	

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
115 120 125

Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
130 135 140

Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
145 150 155 160

Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
165 170 175

Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
180 185 190

Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
195 200 205

Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
210 215 220

His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Thr Leu Gly
225 230 235 240

Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val
245 250 255

Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala
260 265 270

Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg
275 280 285

Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile
290 295 300

Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val
305 310 315 320

Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile
325 330 335

Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Phe Phe Ser
340 345 350

Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu
355 360 365

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser
370 375 380

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn
385 390 395 400

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
405 410 415

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
420 425 430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
450 455 460

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
465 470 475 480

Ile Tyr Ile Lys Leu
485

```
<210> 7
<211> 1380
<212> DNA
<213> Schizosaccharomyces pombe
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<220>
<221> CDS
<222> (1)..(1380)

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<400> 7
atg tca tac aaa ttg gaa aaa gaa gca ttt gtc tca aac ctg acg ggt      48
Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly
   1          5           10          15

```

```
tca agt tcc att gag aca tgt ggc ttg tta tta ata gga att gct tgc 96
Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys
          20           25           30
```

```

aac gtt ttg tgg gta aac atg act gcg aga aac atc tta ccc aaa ggg      144
Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly
          35           40           45

```

aat ctt ggg ttt ctt gtt gag ttt ttc atc ttt tgc tta att cca tta 192
Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu
50 55 60

```

ttt gtc att tac gtt tca tcg aaa gtt ggc gtt ttc act ctt tgc ata      240
Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile
   65           70           75           80

```

```

gcc tct ttt ttg cct tcc ttc gtc ctt cat gtt ata agt cca att aat      288
Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn
          85           90           95

```

```

tgg gat gtg ctg aga aga aaa cct ggt tgt tgt ctt act aaa aaa aat      336
Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn
          100          105          110

```

gaa aat act ttt gat cga cga att gct gga gtc aca ttt tat cgt tct 384
 Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser
 115 120 125

```

caa atg atg ttg gtt act gtc act tgc atc ctg gcc gtt gac ttt acc      432
Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr
   130          135          140

```

ctt ttc ccg agg aga tat gcc aaa gtt gaa acc tgg gga aca tca ctg 480
Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu

145	150	155	160	
atg gat ctt ggt gtt gga tct ttc atg ttt tct tca ggt act gtg gct Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala				528
165	170	175		
gga cgg aaa aat gac att aaa aaa cca aat gcg ttt aaa aat gta ttg Gly Arg Lys Asn Asp Ile Lys Pro Asn Ala Phe Lys Asn Val Leu				576
180	185	190		
tgg aat tct ttc atc ctt ttg att tta gga ttt gcg cgc atg ttt tta Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu				624
195	200	205		
acg aaa agc atc aat tac caa gaa cat gta agc gaa tat ggc atg cat Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His				672
210	215	220		
tgg aac ttt ttc acc cta ggt ttc atg gct ctt ggc gta ttt ttt Trp Asn Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe				720
225	230	235	240	
ttt cgt cgt tct tta aaa aaa gtc tcc tat ttt aat tta gca acc ttc Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe				768
245	250	255		
att act ctt ctt cat cat tgt ttg ctt gtt tta acc cct ttc caa aaa Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys				816
260	265	270		
tgg gca cta tcc gcc ccc aga aca aat att ttg gct cag aat aga gag Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu				864
275	280	285		
ggc att gct tct ctt ccc gga tac att gct att tac ttt tat gga atg Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met				912
290	295	300		
tat acc ggt agt gta gtt ttg gct gat cga cct cta atg tat act aga Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg				960
305	310	315	320	
gct gag tcg tgg aag cgc ttt caa cgt cta tta ttc ccg cta tgc att Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile				1008
325	330	335		
ttg tta gtg ttg tat ctt gtg tct aac ttt ttg tca gtt ggt gtt tct Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser				1056
340	345	350		
cgc cga ctt gct aat acg cct tat gtt gcg aat gtt gcc ttt atc aat Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn				1104
355	360	365		
atg ttt ttt ctt act ata tac ata ctt att gat gcc tat tta ttc cca Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro				1152
370	375	380		
tct tct gtg cca tat gga agt cgc gtc ccc aaa ctg ctt gaa gat gcc Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala				1200
385	390	395	400	

aat aat aat ggc ttg ttg gtg ttt ttg att gct aac gtt tta aca gga		1248	
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly			
405	410	415	
gta gtt aat tta tcg ttc gac acc ctt cat tct agc aat gca aaa ggc		1296	
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly			
420	425	430	
ttg aca atc atg act atg tat ctt ttt att att tgc tat atg gca cat		1344	
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His			
435	440	445	
tgg ctt gct caa cac gga att cgt ttt cgc ctt tag		1380	
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu			
450	455		
<210> 8			
<211> 459			
<212> PRT			
<213> Schizosaccharomyces pombe			
<400> 8			
Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly			
1	5	10	15
Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys			
20	25	30	
Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly			
35	40	45	
Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu			
50	55	60	
Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile			
65	70	75	80
Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn			
85	90	95	
Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Asn			
100	105	110	
Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser			
115	120	125	
Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr			
130	135	140	
Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu			
145	150	155	160
Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala			
165	170	175	
Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu			
180	185	190	
Trp Asn Ser Phe Ile Leu Ile Leu Gly Phe Ala Arg Met Phe Leu			

195

200

205

Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His
210 215 220

Trp Asn Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe
225 230 235 240

Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe
245 250 255

Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys
260 265 270

Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu
275 280 285

Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met
290 295 300

Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg
305 310 315 320

Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile
325 330 335

Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser
340 345 350

Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn
355 360 365

Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro
370 375 380

Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala
385 390 395 400

Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly
405 410 415

Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly
420 425 430

Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His
435 440 445

Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu
450 455

<210> 9
<211> 1576
<212> DNA
<213> Aspergillus fumigatus

<220>
<221> CDS
<222> (31)..(1536)

<400> 9

aagggtcaaa tccccggca ttgagtcaag atg gat cca gat tat aaa gct cgc Met Asp Pro Asp Tyr Lys Ala Arg 1 5	54
aaa gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc Lys Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile 10 15 20	102
aac gcc gtc acc ttg gtc gta tcc gtt ttt ctg tgg tca att Asn Ala Val Thr Leu Val Ala Ser Val Ser Val Phe Leu Trp Ser Ile 25 30 35 40	150
cta caa tct cgc cta tcc ttt ttc aca ccc tac agc gcc gct gcc ctt Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr Ser Ala Ala Ala Leu 45 50 55	198
ctc gtt gat ttc ctg ctc aat gta cta gct atc ttg ttc gca acc act Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile Leu Phe Ala Thr Thr 60 65 70	246
tta tac tct tcg gcg cct ctt ctc aat ctc ctt cta ata tct ccc Leu Tyr Ser Ser Ala Pro Leu Leu Asn Leu Leu Ile Ser Pro 75 80 85	294
gct ctg ctg ata ctc ctc tct acg aaa cgt cct cggt acc ccc gtc aaa Ala Leu Leu Ile Leu Ser Thr Lys Arg Pro Arg Thr Pro Val Lys 90 95 100	342
gcg aaa cct cct cgc cag tcc gct aga gct ggg aaa gat gac tcg aaa Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly Lys Asp Asp Ser Lys 105 110 115 120	390
cat gcg aca gcc ttg cca gag tct cta ccc att cat cca ttt ctc acg His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile His Pro Phe Leu Thr 125 130 135	438
aca tat cgc gcc gcc atg atg gtt atc acg tgc atc gct atc ttg gct Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys Ile Ala Ile Leu Ala 140 145 150	486
gtg gat ttt cgc att ttt cct cgc cga ttc gcc aag gta gaa aac tgg Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala Lys Val Glu Asn Trp 155 160 165	534
ggt aca tca ctc atg gat ctg ggc gtt gga tcg ttt gtc ttt tcg ggc Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser Phe Val Phe Ser Gly 170 175 180	582
gga gta gta tcc gct cgc tca cta ctc aag agc agg acc aat ggc tct Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser Arg Thr Asn Gly Ser 185 190 195 200	630
aaa agg ttg cct ctt gcc aag agg ttg att gcg tcg acg cga cac tct Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala Ser Thr Arg His Ser 205 210 215	678
att cct ctg ctc gtc ctc ggc ctg att cgg cta tac agc gtc aaa ggc Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu Tyr Ser Val Lys Gly 220 225 230	726
ttg gac tat gcg gag cac gtc acc gag tac ggc gta cat tgg aac ttc	774

Leu	Asp	Tyr	Ala	Glu	His	Val	Thr	Glu	Tyr	Gly	Val	His	Trp	Asn	Phe				
235																245			
tgc	tcc	ttt	aca	ttg	ggc	ctt	ttg	cct	ccg	ttc	gtg	gag	gtc	ttc	gac	gcc	822		
Phe	Phe	Thr	Leu	Gly	Leu	Leu	Pro	Pro	Phe	Phe	Val	Glu	Val	Phe	Asp	Ala			
250																260			
ttg	gct	acg	atc	att	ccg	tca	tac	gag	gtt	ctc	tcc	gtg	ggg	atc	gcc	870			
Leu	Ala	Thr	Ile	Ile	Pro	Ser	Tyr	Glu	Val	Leu	Ser	Val	Gly	Ile	Ala				
265																275	280		
gtc	ttg	tat	caa	gtt	gcc	cta	gag	tca	aca	gac	ttg	aaa	agc	tac	atc	918			
Val	Leu	Tyr	Gln	Val	Ala	Leu	Glu	Ser	Thr	Asp	Leu	Lys	Ser	Tyr	Ile				
																285	290	295	
ctc	gtc	tcc	cct	cgt	ggg	cca	agc	tta	ctg	tcc	aag	aat	cgt	gaa	ggc	966			
Leu	Val	Ser	Pro	Arg	Gly	Pro	Ser	Leu	Leu	Ser	Lys	Asn	Arg	Glu	Gly				
																300	305	310	
gtc	tcc	tcc	ttc	tca	ggc	tat	ctc	gct	att	ttt	ctt	gct	ggc	cgt	gct	1014			
Val	Phe	Ser	Phe	Ser	Gly	Tyr	Leu	Ala	Ile	Phe	Leu	Ala	Gly	Arg	Ala				
																315	320	325	
atc	ggc	att	cg	ata	atc	cct	cg	g	ga	act	tct	ttc	tca	aga	agc	cca	1062		
Ile	Gly	Ile	Arg	Ile	Ile	Pro	Arg	Gly	Thr	Ser	Phe	Ser	Arg	Ser	Pro				
																330	335	340	
gaa	cag	gcc	agg	aga	cg	gtc	ctg	atc	agc	ctt	ggc	gtg	caa	g	gc	tta	1110		
Glu	Gln	Ala	Arg	Arg	Arg	Val	Leu	Ile	Ser	Leu	Gly	Val	Gln	Ala	Leu				
																345	350	355	360
gtg	tgg	acc	act	ctt	ttt	gtg	ttg	aa	c	tcc	act	tat	g	cg	at	g	1158		
Val	Trp	Thr	Thr	Leu	Phe	Val	Leu	Asn	Ser	Thr	Tyr	Ala	Met	Gly	Tyr				
																365	370	375	
gga	gct	aat	atc	cct	gtc	tcc	cg	cg	ctc	gct	aa	ac	at	g	cc	tat	gtc	1206	
Gly	Ala	Asn	Ile	Pro	Val	Ser	Arg	Arg	Leu	Ala	Asn	Met	Pro	Tyr	Val				
																380	385	390	
ctt	tgg	gtt	tcg	g	tc	ttc	aa	cc	g	cg	caa	ctg	ttt	gtg	ttc	tgc	ctg	1254	
Leu	Trp	Val	Ser	Ala	Phe	Asn	Thr	Ala	Gln	Leu	Phe	Val	Phe	Cys	Leu				
																395	400	405	
atc	gaa	aca	ctc	tgc	ttt	cct	gca	gtt	cat	cg	aca	ac	act	caa	g	ag	1302		
Ile	Glu	Thr	Leu	Cys	Phe	Pro	Ala	Val	His	Arg	Thr	Thr	Thr	Gln	Glu				
																410	415	420	
agc	gaa	tct	gag	cga	gtc	gat	ttt	gct	ac	g	cg	atc	at	g	tc	gc	1350		
Ser	Glu	Ser	Glu	Arg	Val	Asp	Phe	Ala	Thr	Ser	Arg	Ile	Met	Ser	Ala				
																425	430	435	440
ttc	aat	aag	aa	ag	ctc	g	cg	atc	ttt	ctt	ttg	g	cc	aa	tt	ct	ctg	1398	
Phe	Asn	Lys	Asn	Ser	Leu	Ala	Ile	Phe	Leu	Leu	Ala	Asn	Leu	Leu	Thr				
																445	450	455	
gga	gct	gtg	aat	ctg	agc	atc	tcc	aca	att	gat	g	ct	aa	ca	gc	ca	1446		
Gly	Ala	Val	Asn	Leu	Ser	Ile	Ser	Thr	Ile	Asp	Ala	Asn	Thr	Ala	Gln				
																460	465	470	
gcc	atc	gct	gtt	ctc	att	gga	ta	t	ca	tcc	att	atc	aca	gg	gtt	gct	1494		
Ala	Ile	Ala	Val	Leu	Ile	Gly	Tyr	Ser	Ser	Ile	Ile	Thr	Gly	Val	Ala				

475

480

485

cta gca ttg cat cat gcc aat atc aaa gta ctt cct ttc tag
 Leu Ala Leu His His Ala Asn Ile Lys Val Leu Pro Phe
 490 495 500

1536

ggtatattacg agcaatttgtt ggtgtgttga agatatacg

1576

<210> 10
 <211> 501
 <212> PRT
 <213> Aspergillus fumigatus

<400> 10
 Met Asp Pro Asp Tyr Lys Ala Arg Lys Glu Ala Phe Val Ser Gly Leu
 1 5 10 15
 Ala Gly Gly Ser Ile Leu Glu Ile Asn Ala Val Thr Leu Val Ala Ser
 20 25 30
 Val Ser Val Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe
 35 40 45
 Thr Pro Tyr Ser Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val
 50 55 60
 Leu Ala Ile Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu
 65 70 75 80
 Leu Asn Leu Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr
 85 90 95
 Lys Arg Pro Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala
 100 105 110
 Arg Ala Gly Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser
 115 120 125
 Leu Pro Ile His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val
 130 135 140
 Ile Thr Cys Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg
 145 150 155 160
 Arg Phe Ala Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly
 165 170 175
 Val Gly Ser Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu
 180 185 190
 Leu Lys Ser Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg
 195 200 205
 Leu Ile Ala Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu
 210 215 220
 Ile Arg Leu Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr
 225 230 235 240

Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro
 245 250 255
 Pro Phe Val Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr
 260 265 270
 Glu Val Leu Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu
 275 280 285
 Ser Thr Asp Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser
 290 295 300
 Leu Leu Ser Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu
 305 310 315 320
 Ala Ile Phe Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg
 325 330 335
 Gly Thr Ser Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu
 340 345 350
 Ile Ser Leu Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu
 355 360 365
 Asn Ser Thr Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg
 370 375 380
 Arg Leu Ala Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr
 385 390 395 400
 Ala Gln Leu Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala
 405 410 415
 Val His Arg Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe
 420 425 430
 Ala Thr Ser Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile
 435 440 445
 Phe Leu Leu Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser
 450 455 460
 Thr Ile Asp Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr
 465 470 475 480
 Ser Ser Ile Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile
 485 490 495
 Lys Val Leu Pro Phe
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<210> 11
 <211> 1648
 <212> DNA
 <213> Aspergillus fumigatus

 <220>
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 <222> (122)..(198)

<220>
<221> CDS
<222> (26)..(121)

<220>
<221> CDS
<222> (199) .. (1608)

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agg acc aat ggc tct aaa agg ttg cct ctt gcc aag agg ttg att gcg Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala 200 205 210	735
tcg acg cga cac tct att cct ctg ctc gtc ctc ggc ctg att cgg cta Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu 215 220 225	783
tac agc gtc aaa ggc ttg gac tat gcg gag cac gtc acc gag tac ggc Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly 230 235 240	831
gta cat tgg aac ttc ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg Val His Trp Asn Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val 245 250 255	879
gag gtc ttc gac gcc ttg gct acg atc att ccg tca tac gag gtt ctc Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu 260 265 270 275	927
tcc gtg ggg atc gcc gtc ttg tat caa gtt gcc cta gag tca aca gac Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp 280 285 290	975
ttg aaa agc tac atc ctc gtc tcc cct cgt ggg cca agc tta ctg tcc Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser 295 300 305	1023
aag aat cgt gaa ggc gtc ttc tcc tca ggt tat ctc gcg att ttt Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe 310 315 320	1071
ctt gct ggt cgt gcg atc ggc att cgg ata atc cct cgc gga act tct Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser 325 330 335	1119
ttc tca aga agc cca gaa cag gcc agg aga cgg gtc ctg atc agc ctt Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu Ile Ser Leu 340 345 350 355	1167
ggc gtg caa gcg tta gtg tgg acc act ctt ttt gtg ttg aac tcc act Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr 360 365 370	1215
tat gcg atg gga tac gga gct aat atc cct gtc tcc cgc cgc ctc gct Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala 375 380 385	1263
aac atg ccc tat gtc ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu 390 395 400	1311
ttt gtg ttc tgc ctg atc gaa aca ctc tgc ttt cct gca gtt cat cgg Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg 405 410 415	1359
aca acg act caa gag agc gaa tct gag cga gtc gat ttt gct acg agc	1407

Thr Thr Thr Gln Glu Ser Glu Arg Val Asp Phe Ala Thr Ser
 420 425 430 435
 cga atc atg tcg gcc ttc aat aag aac agt ctc gcg atc ttt ctt ttg 1455
 Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile Phe Leu Leu
 440 445 450
 gcc aat ctt ctg act gga gct gtg aat ctg agc atc tcc aca att gat 1503
 Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser Thr Ile Asp
 455 460 465
 gct aat aca gca gca gct gtt ctc att gga tat tca tcc att 1551
 Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr Ser Ser Ile
 470 475 480
 atc aca ggg gtt gct cta gca ttg cat cat gcc aat atc aaa gta ctt 1599
 Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile Lys Val Leu
 485 490 495
 cct ttc tag ggtatttacg agcaatttgtt ggtgtgttga agatata 1648
 Pro Phe
 500

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aag tcg gcc aaa gag gcc ttt gtc tcg gat aac cca ggt gct tct atc 103
 Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro Gly Ala Ser Ile
 5 10 15 20

tgg agt atc aac gct gtc agc ctg gtc gca ctg gtatgttagct cgttctccga 156
 Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu
 25 30

ggggttctgt catttggaga cgcttattaa ttggatcg ag gcg aca tat gct 210
 Ala Thr Tyr Ala
 35

ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn 40 45 50	258
tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc atc ttc tca Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser 55 60 65	306
act tcg cct ctc gta ttt acc tct ttt ttg tcc att att tcc ctc gct Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile Ser Leu Ala 70 75 80	354
ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt tcg ccc gaa Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu 85 90 95	402
aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat gag gaa cca Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp Glu Glu Pro 100 105 110 115	450
gcg gaa cct gct tct gca gct gga tct gca gca gtc tca cca gta aag Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser Pro Val Lys 120 125 130	498
ctt cta cct tcc caa gtg gcg ttc gct tcc gga tcc cta tta tct ccc Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu Leu Ser Pro 135 140 145	546
gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca gct tca gga Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ala Ser Gly 150 155 160	594
cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg agg tcg cta His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg Arg Ser Leu 165 170 175	642
tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac tcc aag gtc Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp Ser Lys Val 180 185 190 195	690
aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct agg gca acg Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser Arg Ala Thr 200 205 210	738
aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt ttg aca gtg Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe Leu Thr Val 215 220 225	786
tac cga gcg cac atg atg ctc atg act gtt atc tgc atc ttg gcg gta Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile Leu Ala Val 230 235 240	834
gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa gat ttt ggt Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu Asp Phe Gly 245 250 255	882
act agt ctg gtaagcttcc ttccat ggtccagtgc tcaccgtct Thr Ser Leu 260	931

acttgccgta g atg gac gtg ggt gtc ggg tca ttc gtc ttt tcc ctc ggt Met Asp Val Gly Val Gly Ser Phe Val Phe Ser Leu Gly 265 270 275	981
ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act cct acg ccc Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr Pro 280 285 290	1029
tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc ccg tcc ccg Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr Pro Ser Pro 295 300 305	1077
ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc atc ctc gtc Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro Ile Leu Val 310 315 320	1125
ctc ggc ttt ata cgg ttg att atg gtc aag gga tct gat tat cct gag Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp Tyr Pro Glu 325 330 335	1173
cat gtg acg gag tac ggc gtg cac tgg aat ttc ttc ttc acc ctc gca His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Thr Leu Ala 340 345 350 355	1221
ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg cag tgg ctt Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr Gln Trp Leu 360 365 370	1269
cgc tgg agt gtg ctt ggg gta atc atc tct ttg ctg cat cag ctg tgg Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His Gln Leu Trp 375 380 385	1317
tta aca tat tat ctc caa tcc atc gtc ttc tca ttc ggc cgg tca ggt Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly Arg Ser Gly 390 395 400	1365
atc ttt cta gca aac aag gaa ggc ttc tcc tct ctt cct ggt tat ctt Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro Gly Tyr Leu 405 410 415	1413
tcc ata ttt ttg atc ggc ttg tct att gga gat cat gtt tta agg ctc Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val Leu Arg Leu 420 425 430 435	1461
agt tta cca cca aga aga gag agg gtc gtg tca gaa aca aat gaa gag Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr Asn Glu Glu 440 445 450	1509
cat gag cag agt cat ttt gag aga aaa aaa ttg gat ttg att atg gag His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu Ile Met Glu 455 460 465	1557
ttg att gga tat agc tta ggc tgg tgg gca ctc tta gga ggc tgg att Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly Gly Trp Ile 470 475 480	1605
tgg gcc ggc ggg gag gta tcc agg cgt tta gtaagtggac atctttggta Trp Ala Gly Gly Glu Val Ser Arg Arg Leu 485 490	1655
atatttgtacc tatactaatac cctgcataaaa g gcc aac gct cct tat gta ttt	1707

	Ala Asn Ala Pro Tyr Val Phe	
	495	500
tgg gta gcg gca tac aat acc acc ttt ctc ctc ggc tac ctc ctc ctt		1755
Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly Tyr Leu Leu Leu		
505	510	515
acc cac att att cca tct ccc acc tct tcc caa aca tca cca tcg atc		1803
Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr Ser Pro Ser Ile		
520	525	530
tta gtg cct ccc ttg ctc gac gct atg aat aaa aac ggt ctc gcg ata		1851
Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn Gly Leu Ala Ile		
535	540	545
ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat gtg agc atg aag		1899
Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn Val Ser Met Lys		
550	555	560
aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg tta atg ttg tat		1947
Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val Leu Met Leu Tyr		
565	570	575
580		
acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa gga cgg agg atc		1995
Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys Gly Arg Arg Ile		
585	590	595
aag ata tagttaaagt gtttaccatg caggatactg agtatctcgg ttca		2045
Lys Ile		

<210> 13

<211> 1797

<212> DNA

<213> Cryptococcus neoformans

<220>

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<222> (1)..(1794)

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Met Gly Asp Tyr Lys Ser Ala Lys Glu Ala Phe Val Ser Asp Asn Pro		
1	5	10
		15

ggt gct tct atc tgg agt atc aac gct gtc agc ctg gtc gca ctg gcg		96
Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala		
20	25	30

aca tat gct ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc		144
Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu		
35	40	45

ctg aac aac tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc		192
Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr		
50	55	60

atc ttc tca act tcg cct ctc gta ttt acc tct ttt ttg tcc att att		240
Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile		
65	70	75
		80

tcc ctc gct ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser	85	90	95	288
tcg ccc gaa aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp	100	105	110	336
gag gaa cca gcg gaa cct gct tct gca gct gga tct gca gca gtc tca Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser	115	120	125	384
cca gta aag ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu	130	135	140	432
tta tct ccc gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca Leu Ser Pro Asp Pro Thr Ser Pro Met Ser Pro Ser Ser Ser Ser	145	150	155	480
gct tca gga cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg	165	170	175	528
agg tcg cta tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp	180	185	190	576
tcc aag gtc aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser	195	200	205	624
agg gca acg aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe	210	215	220	672
ttg aca gtg tac cga gcg cac atg atg ctc atg act gtt atc tgc atc Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile	225	230	235	720
ttg gcg gta gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu	245	250	255	768
gat ttt ggt act agt ctg atg gac gtg ggt gtc ggg tca ttc gtc ttt Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe	260	265	270	816
tcc ctc ggt ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr	275	280	285	864
cct acg ccc tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr	290	295	300	912
ccg tcc ccg ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc				960

Pro	Ser	Pro	Phe	Thr	Ser	Ile	Leu	Ile	Ser	Leu	Arg	Lys	Ser	Ile	Pro	
305						310				315					320	
atc	ctc	gtc	ctc	ggc	ttt	ata	cgg	ttg	att	atg	gtc	aag	gga	tct	gat	
Ile	Leu	Val	Leu	Gly	Phe	Ile	Arg	Leu	Ile	Met	Val	Lys	Gly	Ser	Asp	
						325				330					335	
tat	cct	gag	cat	gtg	acg	gag	tac	ggc	gtg	cac	tgg	aat	ttc	ttc	ttc	
Tyr	Pro	Glu	His	Val	Thr	Glu	Tyr	Gly	Val	His	Trp	Asn	Phe	Phe	Phe	
						340				345					350	
acc	ctc	gca	ttg	gtt	cct	gtg	ctc	gcc	gtg	ggc	att	cga	cca	ttg	acg	
Thr	Leu	Ala	Leu	Val	Pro	Val	Leu	Ala	Val	Gly	Ile	Arg	Pro	Leu	Thr	
						355				360					365	
cag	tgg	ctt	cgc	tgg	agt	gtg	ctt	ggg	gta	atc	atc	tct	ttg	ctg	cat	
Gln	Trp	Leu	Arg	Trp	Ser	Val	Leu	Gly	Val	Ile	Ile	Ser	Leu	Leu	His	
						370				375					380	
cag	ctg	tgg	tta	aca	tat	tat	ctc	caa	tcc	atc	gtc	ttc	tca	ttc	ggc	
Gln	Leu	Trp	Leu	Thr	Tyr	Tyr	Leu	Gln	Ser	Ile	Val	Phe	Ser	Phe	Gly	
						385				390					400	
cg	tca	gg	atc	ttt	cta	gca	aac	aag	gaa	ggc	ttc	tcc	tct	ttt	cct	
Arg	Ser	Gly	Ile	Phe	Leu	Ala	Asn	Lys	Glu	Gly	Phe	Ser	Ser	Leu	Pro	
						405				410					415	
gg	tat	ctt	tcc	ata	ttt	ttg	atc	ggc	ttg	tct	att	gga	gat	cat	gtt	
Gly	Tyr	Leu	Ser	Ile	Phe	Leu	Ile	Gly	Leu	Ser	Ile	Gly	Asp	His	Val	
						420				425					430	
tta	agg	ctc	agt	tta	cca	cca	aga	aga	gag	agg	gtc	gtg	tca	gaa	aca	
Leu	Arg	Leu	Ser	Leu	Pro	Pro	Arg	Arg	Glu	Arg	Val	Val	Ser	Glu	Thr	
						435				440					445	
aat	gaa	gag	cat	gag	cag	agt	cat	ttt	gag	aga	aaa	aaa	ttg	gat	ttg	
Asn	Glu	Glu	His	Glu	Gln	Ser	His	Phe	Glu	Arg	Lys	Lys	Leu	Asp	Leu	
						450				455					460	
att	atg	gag	ttg	att	gga	tat	agc	tta	ggc	tgg	tgg	gca	ctc	tta	gg	
Ile	Met	Glu	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Trp	Trp	Ala	Leu	Leu	Gly	
						465				470					480	
ggc	tgg	att	tgg	gcc	ggc	ggg	gag	gta	tcc	agg	cgt	tta	gcc	aac	gct	
Gly	Trp	Ile	Trp	Ala	Gly	Gly	Glu	Val	Ser	Arg	Arg	Leu	Ala	Asn	Ala	
						485				490					495	
cct	tat	gta	ttt	tgg	gta	g	g	ca	tac	aat	acc	acc	ttt	ctc	ctc	ggc
Pro	Tyr	Val	Phe	Trp	Val	Ala	Ala	Tyr	Asn	Thr	Thr	Phe	Leu	Leu	Gly	
						500				505					510	
tac	ctc	ctc	ctt	acc	cac	att	att	cca	tct	ccc	acc	tct	tcc	caa	aca	
Tyr	Leu	Leu	Leu	Thr	His	Ile	Ile	Pro	Ser	Pro	Thr	Ser	Ser	Gln	Thr	
						515				520					525	
tca	cca	tcg	atc	tta	gtg	cct	ccc	ttg	ctc	gac	gct	atg	aat	aaa	aac	
Ser	Pro	Ser	Ile	Leu	Val	Pro	Pro	Leu	Leu	Asp	Ala	Met	Asn	Lys	Asn	
						530				535					540	
gg	ctc	gc	at	ttt	ttg	gc	gc	ac	ttg	ctt	aca	gga	ctg	gt	aat	
Gly	Leu	Ala	Ile	Phe	Leu	Ala	Ala	Asn	Leu	Leu	Thr	Gly	Leu	Val	Asn	

545

550

555

560

gtg agc atg aag aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg 1728
 Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
 565 570 575

tta atg ttg tat acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa 1776
 Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys
 580 585 590

gga cgg agg atc aag ata tag 1797
 Gly Arg Arg Ile Lys Ile
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<210> 14
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<212> PRT
<213> Cryptococcus neoformans

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Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala
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Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu
 35 40 45

Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr
 50 55 60

Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile
 65 70 75 80

Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser
 85 90 95

Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp
 100 105 110

Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser
 115 120 125

Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu
 130 135 140

Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser
 145 150 155 160

Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg
 165 170 175

Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp
 180 185 190

Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser
 195 200 205

Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe

210	215	220
Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile		
225	230	235
Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu		
245	250	255
Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe		
260	265	270
Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr		
275	280	285
Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr		
290	295	300
Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro		
305	310	315
Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp		
325	330	335
Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe		
340	345	350
Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr		
355	360	365
Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His		
370	375	380
Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly		
385	390	395
Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro		
405	410	415
Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val		
420	425	430
Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr		
435	440	445
Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu		
450	455	460
Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly		
465	470	475
Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala		
485	490	495
Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly		
500	505	510
Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr		
515	520	525
Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn		

530

535

540

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn
545 550 555 560

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
565 570 575

Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys
 580 585 590

Gly Arg Arg Ile Lys Ile
595

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<212> DNA
<213> Artificial sequence
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<220>
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ggaattcatg tcgactttaa aacagaaaaa aqagg

35

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<212> DNA
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<220>
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gcatcgattt atagcttaat qaataattctt tttctatac

39

<210> 17
<211> 60
<212> DNA
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<210> 18
<211> 60
<212> DNA
<213> *Saccharomyces cerevisiae*

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